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RAW SEQUENCE LISTING

DATE: 03/25/2002 P.S
TIME: 10:49:38

PATENT APPLICATION: US/09/978,274A

Input Set : A:\9341-028-999.txt

Output Set: N:\CRF3\03252002\I978274A.raw

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5 <110> APPLICANT: Thomas, Christopher
7      McPherson, Michael
9      Atkinson, Howard
11     Neelam, Anil
15 <120> TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
19 <130> FILE REFERENCE: 9341-028
23 <140> CURRENT APPLICATION NUMBER: 09/978,274A
25 <141> CURRENT FILING DATE: 2001-10-15
29 <150> PRIOR APPLICATION NUMBER: 0025225.4
31 <151> PRIOR FILING DATE: 2000-10-14
35 <160> NUMBER OF SEQ ID NOS: 32
39 <170> SOFTWARE: PatentIn version 3.1
43 <210> SEQ ID NO: 1
45 <211> LENGTH: 945
47 <212> TYPE: DNA
49 <213> ORGANISM: Phytolacca americana
53 <400> SEQUENCE: 1
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58 gccaccttta tggaatctct tcgtaatcaa gcgaaagatc caaaactaaa atgctatggc      180
60 ataccaatgc tacctgatac taattcgacc cctaagtact tattggttaa gctccaaggt      240
62 gcaaacctaa aaaccattac actaatgctg agacgaaata acttatacgt gatgggctat      300
64 tctgatccct tcaatggcaa taagtgtcgt taccatatat ttaatgatat tacaagcacc      360
66 gaacgcactg atgtggagaa tactctttgc tcaagttcta gttctcgtgt tgcaatgtcc      420
68 attaactaca atagcttata tccgaccatg gaaaagaaag cagaagtaaa ctcaagaaat      480
70 caagtccaat tgggaattca aatactcagc agtgacattg gaaaaatctc tggagttgat      540
72 tcattccctg taaaaactga ggcttttttt ctactggtag ccatccaaat ggtttcagag      600
74 gcagcgcgat tcaagtacat agagaaccaa gtcaagacta attttaatag agcattctac      660
76 cctgatccca aagtaattaa tttggaggag aagtggggca aaatctctga ggcaattcac      720
78 aatgccaaga atggggcttt acccaaacca cttgagctag tggatgccaa aggtaccaag      780
80 tggatagttc ttagagtgga tgaaatcaat cgtgatgtgg cactccttaa gtacgttaat      840
82 ggaacctgtc agacaactta ccaaaatgcc atgttctctc aagttataat ttctacttat      900
84 tataattata tgtctaattc tggatgatcta tttgaaggat tctaa      945
87 <210> SEQ ID NO: 2
89 <211> LENGTH: 314
91 <212> TYPE: PRT
93 <213> ORGANISM: Phytolacca americana
97 <400> SEQUENCE: 2
99 Met Lys Val Met Leu Val Val Val Val Thr Leu Ile Ala Trp Leu Ile
100 1          5          10          15
103 Ala Ala Pro Thr Ser Thr Cys Ala Ile Asn Thr Ile Thr Phe Asp Ala
104          20          25          30
107 Gly Asn Ala Thr Ile Asn Lys Tyr Ala Thr Phe Met Glu Ser Leu Arg

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108          35          40          45
111 Asn Gln Ala Lys Asp Pro Lys Leu Lys Cys Tyr Gly Ile Pro Met Leu
112          50          55          60
115 Pro Asp Thr Asn Ser Thr Pro Lys Tyr Leu Leu Val Lys Leu Gln Gly
116 65          70          75          80
119 Ala Asn Leu Lys Thr Ile Thr Leu Met Leu Arg Arg Asn Asn Leu Tyr
120          85          90          95
123 Val Met Gly Tyr Ser Asp Pro Phe Asn Gly Asn Lys Cys Arg Tyr His
124          100          105          110
127 Ile Phe Asn Asp Ile Thr Ser Thr Glu Arg Thr Asp Val Glu Asn Thr
128          115          120          125
131 Leu Cys Ser Ser Ser Ser Ser Arg Val Ala Met Ser Ile Asn Tyr Asn
132          130          135          140
135 Ser Leu Tyr Pro Thr Met Glu Lys Lys Ala Glu Val Asn Ser Arg Asn
136 145          150          155          160
139 Gln Val Gln Leu Gly Ile Gln Ile Leu Ser Ser Asp Ile Gly Lys Ile
140          165          170          175
143 Ser Gly Val Asp Ser Phe Pro Val Lys Thr Glu Ala Phe Phe Leu Leu
144          180          185          190
147 Val Ala Ile Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu
148          195          200          205
151 Asn Gln Val Lys Thr Asn Phe Asn Arg Ala Phe Tyr Pro Asp Pro Lys
152          210          215          220
155 Val Ile Asn Leu Glu Glu Lys Trp Gly Lys Ile Ser Glu Ala Ile His
156 225          230          235          240
159 Asn Ala Lys Asn Gly Ala Leu Pro Lys Pro Leu Glu Leu Val Asp Ala
160          245          250          255
163 Lys Gly Thr Lys Trp Ile Val Leu Arg Val Asp Glu Ile Asn Arg Asp
164          260          265          270
167 Val Ala Leu Leu Lys Tyr Val Asn Gly Thr Cys Gln Thr Thr Tyr Gln
168          275          280          285
171 Asn Ala Met Phe Ser Gln Val Ile Ile Ser Thr Tyr Tyr Asn Tyr Met
172          290          295          300
175 Ser Asn Leu Gly Asp Leu Phe Glu Gly Phe
176 305          310
179 <210> SEQ ID NO: 3
181 <211> LENGTH: 792
183 <212> TYPE: DNA
185 <213> ORGANISM: Phytolacca americana
189 <400> SEQUENCE: 3
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192 atggaatctc ttcgtaatca agcgaaagat ccaaaactaa aatgctatgg cataccaatg      120
194 ctacctgata ctaattcgac ccctaagtac ttattgggta agctccaagg tgcaaaccta      180
196 aaaaccatta cactaatgct gagacgaaat aacttatacg tgatgggcta ttctgatccc      240
198 ttcaatggca ataagtgtcg ttaccatata tttaatgata ttacaagcac cgaacgcact      300
200 gatgtggaga atactctttg ctcaagttct agttctcgtg ttgcaatgtc cattaactac      360
202 aatagcttat atccgaccat ggaaaagaaa gcagaagtaa actcaagaaa tcaagtccaa      420
204 ttgggaattc aaatactcag cagtgcattt ggaaaaatct ctggagttga ttcattccct      480
206 gtaaaaaactg aggcctttttt tctactggta gccatccaaa tggtttcaga ggcagcgca      540

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208 ttcaagtaca tagagaacca agtcaagact aattttaata gagcattcta ccctgatccc      600
210 aaagtaatta acttggagga gaagtggggc aaaatctctg aggcaattca caatgccaaag      660
212 aatggggctt tacccaaacc acttgagcta gtggatgcca aaggtaccaa gtggatagtt      720
214 cttagagtgg atgaaatcaa tcgtgatgtg gcactcctta agtacgttaa tggaacctgt      780
216 cagacaactt aa      792
219 <210> SEQ ID NO: 4
221 <211> LENGTH: 263
223 <212> TYPE: PRT
225 <213> ORGANISM: Phytolacca americana
229 <400> SEQUENCE: 4
231 Met Ile Asn Thr Ile Thr Phe Asp Ala Gly Asn Ala Thr Ile Asn Lys
232 1 5 10 15
235 Tyr Ala Thr Phe Met Glu Ser Leu Arg Asn Gln Ala Lys Asp Pro Lys
236 20 25 30
239 Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asp Thr Asn Ser Thr Pro
240 35 40 45
243 Lys Tyr Leu Leu Val Lys Leu Gln Gly Ala Asn Leu Lys Thr Ile Thr
244 50 55 60
247 Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser Asp Pro
248 65 70 75 80
251 Phe Asn Gly Asn Lys Cys Arg Tyr His Ile Phe Asn Asp Ile Thr Ser
252 85 90 95
255 Thr Glu Arg Thr Asp Val Glu Asn Thr Leu Cys Ser Ser Ser Ser Ser
256 100 105 110
259 Arg Val Ala Met Ser Ile Asn Tyr Asn Ser Leu Tyr Pro Thr Met Glu
260 115 120 125
263 Lys Lys Ala Glu Val Asn Ser Arg Asn Gln Val Gln Leu Gly Ile Gln
264 130 135 140
267 Ile Leu Ser Ser Asp Ile Gly Lys Ile Ser Gly Val Asp Ser Phe Pro
268 145 150 155 160
271 Val Lys Thr Glu Ala Phe Phe Leu Leu Val Ala Ile Gln Met Val Ser
272 165 170 175
275 Glu Ala Ala Arg Phe Lys Tyr Ile Glu Asn Gln Val Lys Thr Asn Phe
276 180 185 190
279 Asn Arg Ala Phe Tyr Pro Asp Pro Lys Val Ile Asn Leu Glu Glu Lys
280 195 200 205
283 Trp Gly Lys Ile Ser Glu Ala Ile His Asn Ala Lys Asn Gly Ala Leu
284 210 215 220
287 Pro Lys Pro Leu Glu Leu Val Asp Ala Lys Gly Thr Lys Trp Ile Val
288 225 230 235 240
291 Leu Arg Val Asp Glu Ile Asn Arg Asp Val Ala Leu Leu Lys Tyr Val
292 245 250 255
295 Asn Gly Thr Cys Gln Thr Thr
296 260
299 <210> SEQ ID NO: 5
301 <211> LENGTH: 465
303 <212> TYPE: DNA
305 <213> ORGANISM: Phytolacca americana
309 <400> SEQUENCE: 5

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310 atgataaata cgatcacctt tgatgctgga aatgccacca ttaacaaata tgccaccttt      60
312 atggaatctc ttcgtaatca agcgaaagat ccaaaactaa aatgctatgg cataccaatg      120
314 ctacctgata ctaattcgac ccctaagtac ttattggtta agctccaagg tgcaaaccta      180
316 aaaaccatta cactaatgct gagacgaaat aacttatacg tgatgggcta ttctgatccc      240
318 ttcaatggca ataagtgtcg ttaccatata tttaatgata ttacaagcac cgaacgcact      300
320 gatgtggaga atactctttg ctcaagttct agttctcgtg ttgcaatgtc cattaactac      360
322 aatagcttat atccgaccat ggaaaagaaa gcagaagtaa actcaagaaa tcaagtccaa      420
324 ttgggaattc aaatactcag cagtgcattt ggaaaaatct cttaa                      465

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327 <210> SEQ ID NO: 6

329 <211> LENGTH: 154

331 <212> TYPE: PRT

333 <213> ORGANISM: *Phytolacca americana*

337 <400> SEQUENCE: 6

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339 Met Ile Asn Thr Ile Thr Phe Asp Ala Gly Asn Ala Thr Ile Asn Lys
340 1          5          10          15
343 Tyr Ala Thr Phe Met Glu Ser Leu Arg Asn Gln Ala Lys Asp Pro Lys
344          20          25          30
347 Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asp Thr Asn Ser Thr Pro
348          35          40          45
351 Lys Tyr Leu Leu Val Lys Leu Gln Gly Ala Asn Leu Lys Thr Ile Thr
352          50          55          60
355 Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser Asp Pro
356 65          70          75          80
359 Phe Asn Gly Asn Lys Cys Arg Tyr His Ile Phe Asn Asp Ile Thr Ser
360          85          90          95
363 Thr Glu Arg Thr Asp Val Glu Asn Thr Leu Cys Ser Ser Ser Ser Ser
364          100         105         110
367 Arg Val Ala Met Ser Ile Asn Tyr Asn Ser Leu Tyr Pro Thr Met Glu
368          115         120         125
371 Lys Lys Ala Glu Val Asn Ser Arg Asn Gln Val Gln Leu Gly Ile Gln
372          130         135         140
375 Ile Leu Ser Ser Asp Ile Gly Lys Ile Ser
376 145         150

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379 <210> SEQ ID NO: 7

381 <211> LENGTH: 333

383 <212> TYPE: DNA

385 <213> ORGANISM: *Phytolacca americana*

389 <400> SEQUENCE: 7

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390 atgggagtgt attcattccc tgtaaaaact gaggtttttt ttctactggt agccatccaa      60
392 atggtttcag aggcagcgcg attcaagtac atagagaacc aagtcaagac taattttaat      120
394 agagcattct accctgatcc caaagtaatt aatttgaggg agaagtgggg caaatctctt      180
396 gaggaatttc acaatgccaa gaatgggggt ttacccaaac cacttgagct agtggatgcc      240
398 aaaggtacca agtggatagt tcttagagtg gatgaaatca atcgtgatgt ggcactcctt      300
400 aagtacgtta atggaacctg tcagacaact taa                      333

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403 <210> SEQ ID NO: 8

405 <211> LENGTH: 110

407 <212> TYPE: PRT

409 <213> ORGANISM: *Phytolacca americana*

413 <400> SEQUENCE: 8

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
Input Set : A:\9341-028-999.txt

Output Set: N:\CRF3\03252002\I978274A.raw

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415 Met Gly Val Asp Ser Phe Pro Val Lys Thr Glu Ala Phe Phe Leu Leu
416 1          5          10          15
419 Val Ala Ile Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu
420          20          25          30
423 Asn Gln Val Lys Thr Asn Phe Asn Arg Ala Phe Tyr Pro Asp Pro Lys
424          35          40          45
427 Val Ile Asn Leu Glu Glu Lys Trp Gly Lys Ile Ser Glu Ala Ile His
428          50          55          60
431 Asn Ala Lys Asn Gly Ala Leu Pro Lys Pro Leu Glu Leu Val Asp Ala
432 65          70          75          80
435 Lys Gly Thr Lys Trp Ile Val Leu Arg Val Asp Glu Ile Asn Arg Asp
436          85          90          95
439 Val Ala Leu Leu Lys Tyr Val Asn Gly Thr Cys Gln Thr Thr
440          100          105          110
443 <210> SEQ ID NO: 9
445 <211> LENGTH: 43
447 <212> TYPE: DNA
449 <213> ORGANISM: Unknown
453 <220> FEATURE:
455 <223> OTHER INFORMATION: PPS1BF primer
457 <400> SEQUENCE: 9
458 actcgagtct agaggattca tgaaggtgat gcttgtagtt gtg
461 <210> SEQ ID NO: 10
463 <211> LENGTH: 43
465 <212> TYPE: DNA
467 <213> ORGANISM: Unknown
471 <220> FEATURE:
473 <223> OTHER INFORMATION: PPS2SR primer
475 <400> SEQUENCE: 10
476 gactagtgtc gacgagctct tagaatcctt caaatagatc acc
479 <210> SEQ ID NO: 11
481 <211> LENGTH: 48
483 <212> TYPE: DNA
485 <213> ORGANISM: Unknown
489 <220> FEATURE:
491 <223> OTHER INFORMATION: PS1BF primer
493 <400> SEQUENCE: 11
494 gctcgagtct agaggattca tgataaatac gatcaccttt gatgctgg
497 <210> SEQ ID NO: 12
499 <211> LENGTH: 47
501 <212> TYPE: DNA
503 <213> ORGANISM: Unknown
507 <220> FEATURE:
509 <223> OTHER INFORMATION: PS2SR primer
511 <400> SEQUENCE: 12
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515 <210> SEQ ID NO: 13
517 <211> LENGTH: 52
519 <212> TYPE: DNA

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 Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/978,274A

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Input Set : A:\9341-028-999.txt

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L:905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28

L:955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/978,274

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOF

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.